

10/609962

Fig. 1

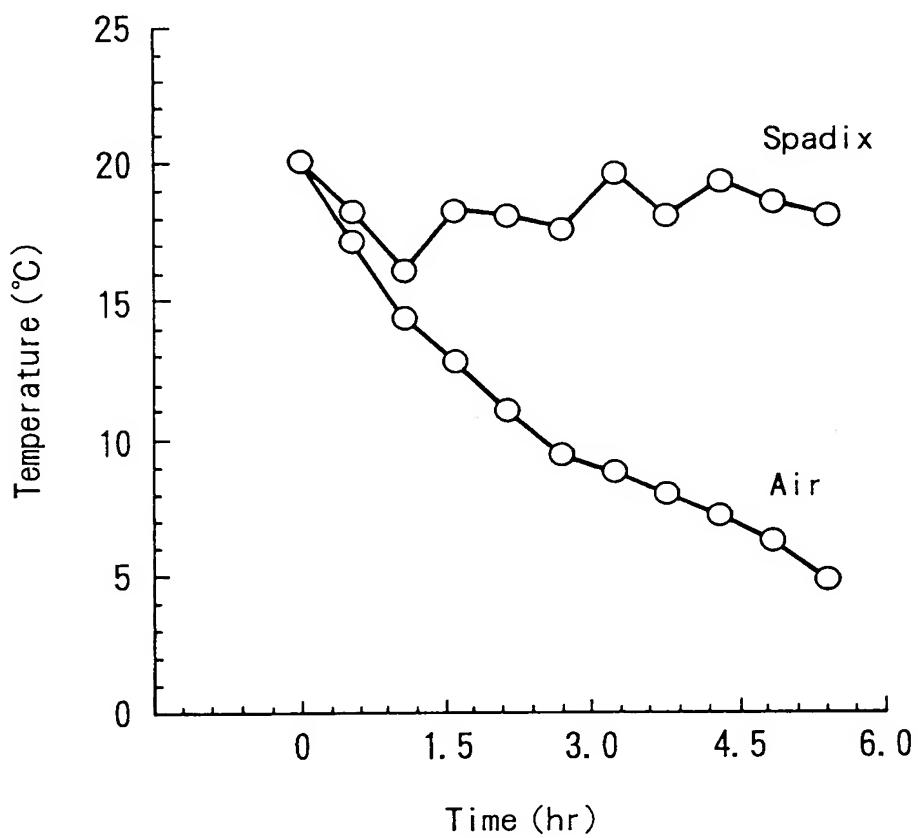


Fig. 2

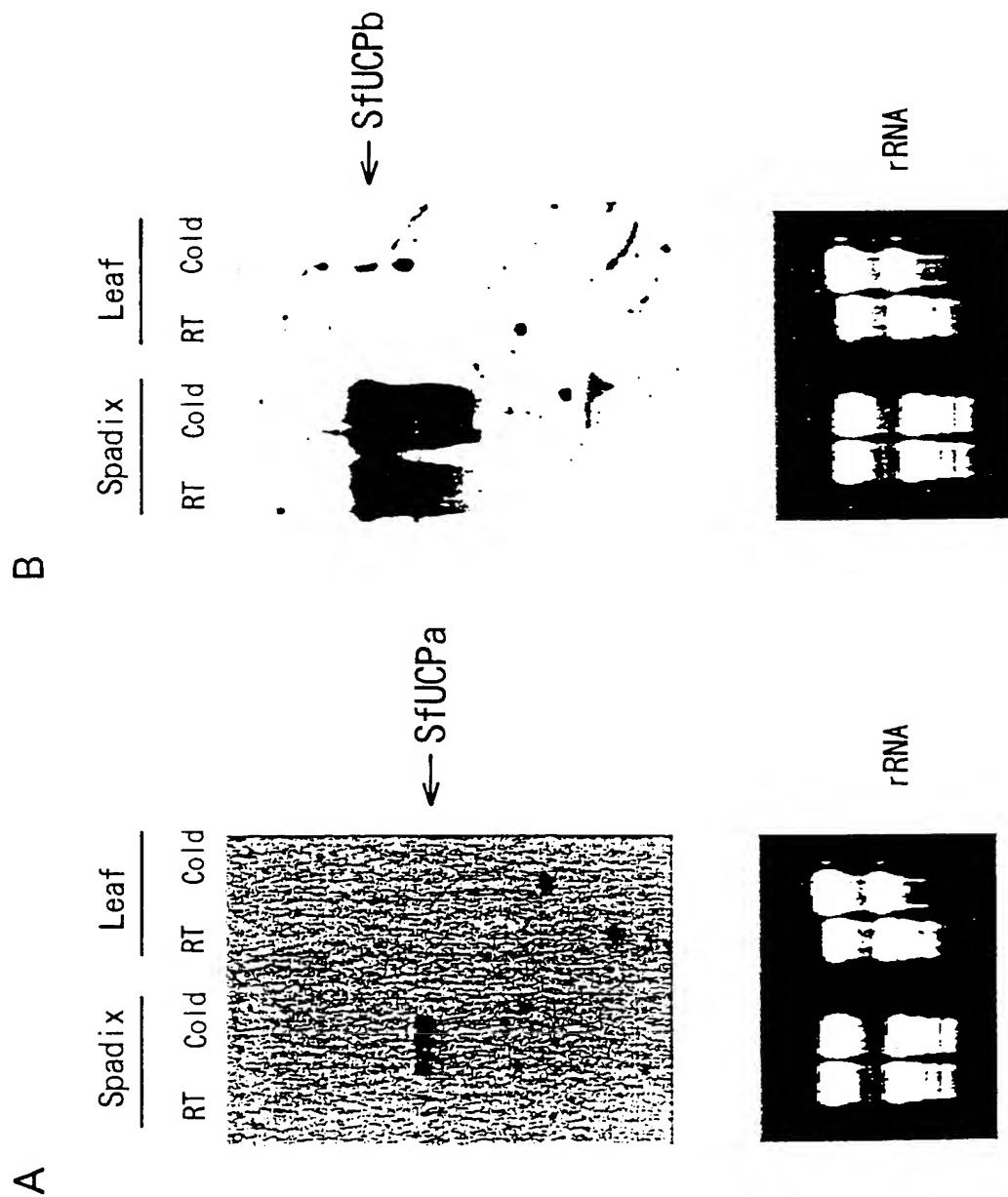


Fig. 3 Top

		I		II
SfUCPA	1	--MGDHGPRTEISFAGSSR-AAFAACFAELCTP	PLOTAKVRQLQKRAVITGDV-VALPKY	56
SfUCPB	1	--MGDHGPRTEISFAGSSR-AAFAACFAELCTP	PLOTAKVRQLQKRAVITGDV-VALPKY	56
StUCP	1	MCGGDHGCKSDISFAGIFASSAAACFAEACTIP	PLOTAKVRQLQKRAVEGDLG-LALPKY	59
AtPUMP	1	--MVAAGKSDLSLPKTFACSAFAACVGEVCTIP	PLOTAKVRQLQKSAFTLAGDVTLPKY	57
human UCP1	1	-MGGLTASDVRHPTLGVQLFSAPIAACIADVITP	PLOTAKVRQLQVQGECP----TSSVIRY	55
human UCP2	1	-KVGFKAATDVPPTATVKFLGACTAACIADLITP	PLOTAKVRQLQIIGESSQGPVRATASAQY	59
human UCP3	1	-KVGLKPSDVPPTMAVKFLGACTAACFADLVTHP	PLOTAKVRQLQICQGENQ-AVQTARLVQY	58

SfUCPA	57	RGAAGLGTVAIAREEGLSALWKGRIVPGCLHRQCCLFGGLRIGLYEPVVKSFYVG--DNFTVGDI P	114	
SfUCPB	57	RGMILGTVAIAREEGLSALWKGRIVPGCLHRQCCLFGGLRIGLYEPVVKSFYVG--DNFTVGDI P	114	
StUCP	60	RGLLGTVGTLAKEEGLASLWKGRIVPGCLHRQCCLFGGLRIGMYEPVVKNLIVFTGKDFTVGDP	117	
AtPUMP	58	RGLLGTVGTLAREEGLRSLWKGRIVPGCLHRQCCLFGGLRIGMYEPVVKNLIVFTGKDFTVGDP	117	
human UCP1	56	KGVLTGTTAVVKTEGRKKLYSGLPAGLQRQISSASLRIGLYDTVQEFLTA---GKETAPS	112	
human UCP2	60	RGVNGTILTMRVTRERSLYNGLVAGLQRQMSFAASVRIIGLYDSVTKQFYT----KGSEHAS	115	
human UCP3	59	RGVLTGTTLMVRTEGRCSPYNGLVAGLQRQMSFAASIRIGLYDSVTKQVYTP---KGADNSS	115	

Fig. 3 Middle

		III	IV	V
SfUCPA	115	LSRKILLAGLITGALAIIVANPTDLVVRVLQSEGKLP PG--VPRRYSGALLNAY--STIVRKE	171	
SfUCPB	115	LSRKILLAGLITGALAIIVANPTDLVVRVLQSEGKLP PG--VPRRYSGALLNAY--STIVRRE	171	
StUCP	118	LSKCKILLAGLITGALGITIANPTDLVVRVLQAECKLIPAG--VPRRYSGALLNAY--STIVRQE	174	
AtPUMP	118	LSKCKILLAGLITGALGIMVANPTDLVVRVLQAECKLAAAG--APRRYSGALLNAYFTSTIVRQE	176	
human UCP1	113	LGSKKILLAGLITGGVAVFIGQPTEVVKVRLQAQSHLHG--IKPRYTGTYNAY--RIIATE	168	
human UCP2	116	IGSRLLAGSTTGALAVAVAQPTDVVKVRFQAQARAG---GGRRYQSTVNAY--KTLAREE	170	
human UCP3	116	LTTRILAGCTTGAMAVTCAQPTDVVKVRFQASIHLGPSRSDRKYSGTMDAY--RTLAREE	173	
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SfUCPA	172	GIGALKITGLGPNTIARNAIINAAELASYDQVTKQTILKLGFSNDNIFTILAG--LGAGFFA	229	
SfUCPB	172	GIGALKITGLGPNTIARNAIINAAELASYDQVKQ-----	203	
StUCP	175	GVRAALKITGLGPNTICRNAIINAAELASYDQVKEAVLRIPGFTDNVVTHILAG--LGAGFFA	232	
AtPUMP	177	GVRAALKITVLPGPNVARNAIINAAELASYDQVKEETILKIPGFTDNVVTHILSGLEFTGAGFFA	216	
human UCP1	169	GLTGLWKGTTPNLMRSVIINCTELVTYDLIKEAFVKNNILADDVPCHLVSA--LIAGFFA	226	
human UCP2	171	GFRGLWKGTTSPNVARNAIIVNCAEIVTCHEFTSA--FGAGFFCT	228	
human UCP3	174	GVRGLWKGTTPNIMRNIAIVNCAEIVTCHEFTSA--FGAGFFCA	231	
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Fig.3 Down

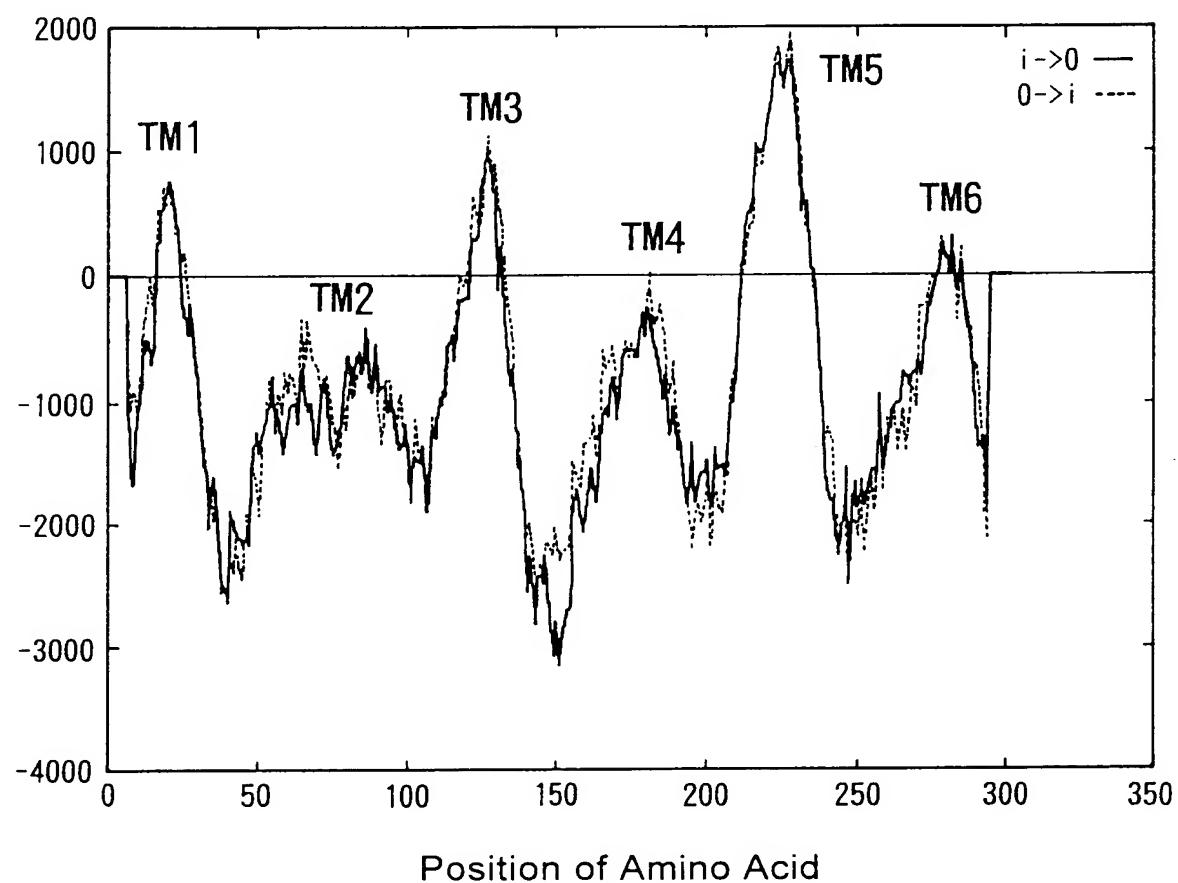
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SfUCPA	230	VCIGSPVDVVKSRMKGDS--AYKSTIFDCFIRTLKNDGLLAFYRKGFIPNFGRLG--SWNVI	285
SfUCPB	204	-----MKSRMKGDS--AYKSTIFDCFIRTLKNDGPLAFYRKGFIPNFGRLG--SWNVI	250
StUCP	233	VCIGSPVDVVKSRMKGDS--AYKNTILDCFVKTILKNDGPLAFYRKGFIPNFGRLG--SWNVI	288
AtPUMP	237	VCIGSPVDVVKSRMKGDSG--AYKGTIDCFVKTILKSDGPMAFYRKGFIPNFGRLGSFTNVI	295
human UCP1	227	TAMSSPVDVVKTRHINSPPGQYKSVPNCAMKVFTNEGPTAFKGLVPSFLRG--SWNVI	284
human UCP2	229	TVIASPVDVVKTRKMNSALGQYSSAGBCALTMLQKEGPRAFYRKGFMPSFTRLG--SWNIV	286
human UCP3	232	TCVRSAPVDVVKTRHANSPPGQIFS2LDCMIRKVAQEGLTAFYRKGFIPSFTRLG--SWNIV	289

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SfUCPA	286	MFLTLEQVTKFTIKEVPN-----	303
SfUCPB	251	MFLTLEQVTKFTIKEVPN-----	268
StUCP	289	MFLTLEQAKKFTVKSLESP-----	306
AtPUPP	296	MFLTLEQAKKYRELDASKPN--	316
human	UCP1	MFVCFEQLKRELSSRQTHDCAT	307
human	UCP2	MFVTTTEQLKRALMAACTSREAPF	309
human	UCP3	MFVTTTCOOLKBALMTCYQWTFEEDE	212

Fig.4



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Fig.5

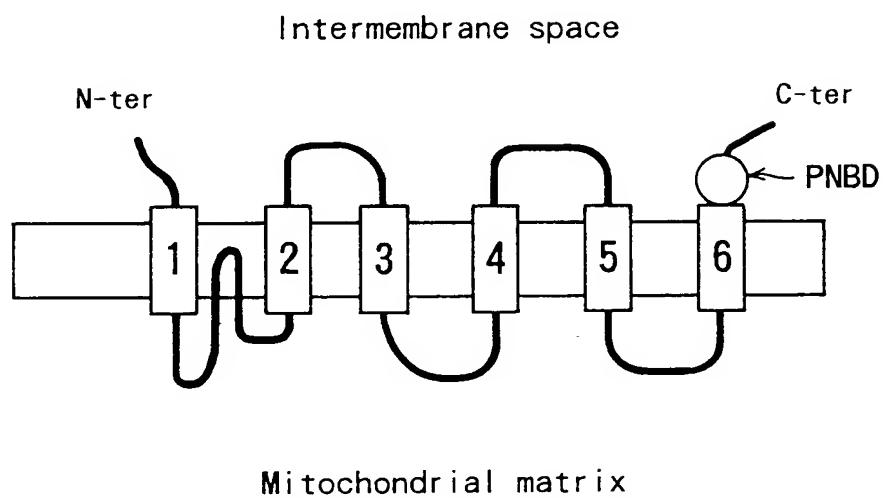
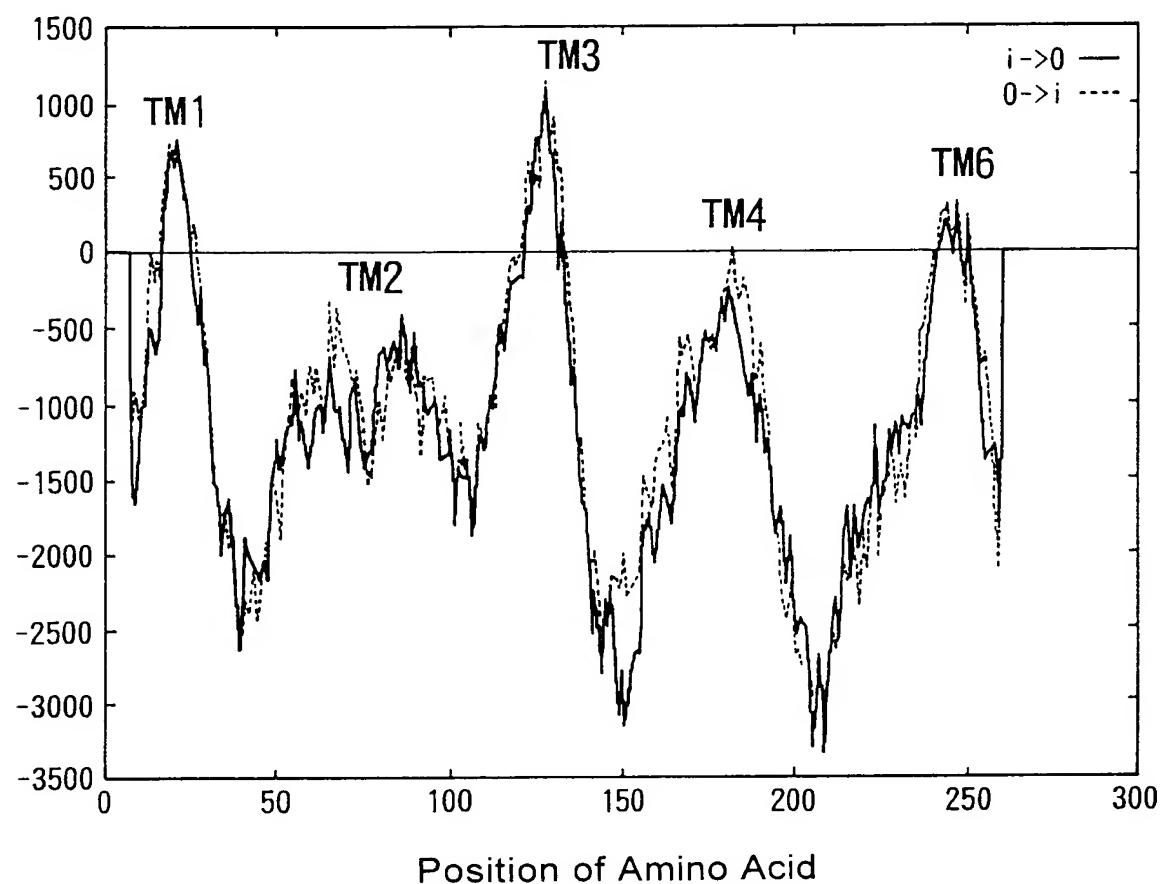


Fig.6



Position of Amino Acid

Fig.7

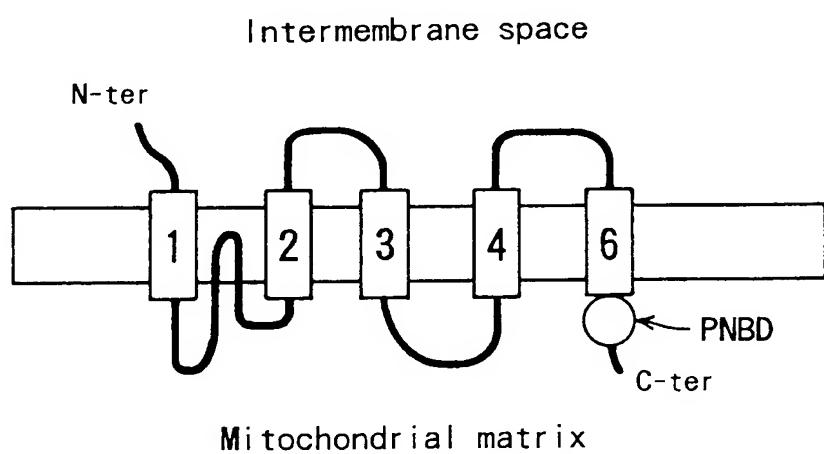


Fig.8

